

SEQUENZ LISTING

GENERAL INFORMATION:

APPLICANT:

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STREET: Bergstraße 85
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COUNTRY: Deutschland
POSTCODE: 64319

VERTRETER:

NAME: Dr. Ulrike Rudolph
STREET: In der Schanz 10
CITY: Schriesheim
FEDERAL STATE: Baden-Württemberg
COUNTRY: Deutschland
POSTCODE: 69198
AGENT NUMBER: 246 263
FILE NUMBER: km-3#

TELEKOMMUNICATION:

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TITEL OF INVENTION:

Regulatory Protein pKe#83 from humanen Keratinocytes

NUMBER OF SEQUENCES: 8

COMPUTER READABLE VERSION:

DATA CARRIER: Diskette
COMPUTER: IBM-kompatible PC
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft WORD for Windows 6.0

INFORMATION OF SEQ ID NO:1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2667 base pairs
SPECIES: desoxyribonucleic acid
TOPOLOGY: linear

MOLECULE SPECIES: cDNA

HYPOTHETICALLY: no

ANTI-SENSE: no

NATURAL ORIGIN :

ORGANISM: Homo sapiens
STRAIN: caucasian
DEVELOPMENTAL STAGE: adult
CELL TYPE: epidermal keratinocyte

DIRECT ORIGIN: cDNA from keratinocytes

FEATURE:

NAME/KEY: coding sequence for the
regulatory protein pKe#83
from human Keratinocytes

POSITION: from 1 to 2667
METHOD OF INVESTIGATION: cDNA-Sequencing

SEQ ID NO: 1

```
1  GTTTTGTAG GCAAAAAGAG ACTATTGAAA GCTGAGACTT TAGAATTGAG
51  TGA CTTATAT GTTAGTGATA AGAAGAAGGA TATGTCTCCA CCCTTTATTT
101 GTGAGGAGAC AGATGAACAA AAGCTTCAAA CTCTAGACAT CGGTAGTAAC
151 TTGGAGAAAG AAAAATTAGA GAATTCCAGA TCCTTAGAAT GCAGATCAGA
201 TCCAGAATCT CCTATCAAAA AAACAAGTTT ATCTCCTACT TCTAAACTTG
251 GATACTCATA TAGTAGAGAT CTAGACCTTG CTAAGAAAAA ACATGCTTCC
301 CTGAGGCAGA CGGAGTCTGA TCCAGATGCT GATAGAACCA CTTTAAATCA
351 TGCAGATCAT TCATCAAAAA TAGTCCAGCA TCGATTGTTA TCTAGACAAG
401 AAGAACTTAA GGAAAGAGCA AGAGTTCTGC TTGAGCAAGC AAGAAGAGAT
451 GCAGCCTTAA AGGCGGGGAA TAAGCACAAT ACCAACACAG CCACCCCAT
501 CTGCAACAGG CAGCTAAGTG ATCAGCAAGA TGAAGAGCGA CGTCGGCAGC
551 TGAGAGAGAG AGCTCGTCAG CTAATAGCAG AAGCTCGATC TGGAGTGAAG
601 ATGTCAGAAC TTCCCAGCTA TGGTGAAATG GCTGCAGAAA AGTTGAAAGA
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651	AAGGTCAAAG	GCATCTGGAG	ATGAAAATGA	TAATATTGAG	ATAGATACTA
701	ACGAGGAGAT	CCCTGAAGGC	TTTGTGTAG	GAGGTGGAGA	TGAACCTACT
751	AACTTAGAAA	ATGACCTTGA	TACTCCCGAA	CAAAACAGTA	AGTTGGTGGA
801	CTTGAAGCTG	AAGAAGCTCC	TAGAAGTTCA	GCCACAGGTG	GCAAATTCAC
851	CCTCCAGTGC	TGCCCAGAAA	GCTGTAACTG	AGAGCTCAGA	GCAGGACATG
901	AAAAGTGCCA	CAGAAGATCT	CCGGACTGAA	CGATTACAAA	AAACAACAGA
951	ACGTTTTAGA	AATCCTGTTG	TGTTTCAGCAA	AGATTCTACA	GTCAGAAAAA
1001	CTCAACTTCA	GTCTTTTCAGC	CAATATATTG	AGAATAGACC	AGAGATGAAA
1051	AGGCAGAGAT	CAATACAGGA	AGATACAAAG	AAAGGAAATG	AGGAGAAGGC
1101	AGCGATAACT	GAAACTCAGA	GGAAGCCATC	AGAAGATGAA	GTGCTTAATA
1151	AAGGGTTCAA	AGACACCAGT	CAGTATGTAG	TAGGAGAATT	GGCAGCACTA
1201	GAGAAATGAGC	AAAAGCAAAT	TGACACCCGT	GCCGCGCTGG	TGGAGAAGCG
1251	CCTTCGCTAT	CTCATGGACA	CAGGAAGGAA	CACAGAAGAA	GAAGAAGCTA
1301	TGATGCAGGA	ATGGTTTATG	TTAGTTAATA	AGAAAAATGC	CTTAATAAGG
1351	AGAATGAATC	AGCTCTCTCT	TCTGGAAAAA	GAACATGATT	TAGAACGACG
1401	GTATGAGCTG	CTGAACCGGG	AATTGAGGGC	AATGCTAGCC	ATTGAAGACT
1451	GGCAGAAGAC	CGAGGCCCGAG	AAGCGACGCG	AACAGCTTCT	GCTAGATGAG
1501	CTGGTGGCCC	TGGTGAACAA	GCGCGATGCG	CTCGTCAGGG	ACCTGGACGC
1551	GCAGGAGAAG	CAGGCCGAAG	AAGAAGATGA	GCATTTGGAG	CGAACTCTGG
1601	AGCAAAACAA	AGGCAAGATG	GCCAAGAAAG	AGGAGAAATG	TGTTCTTCAG
1651	TAGCCATCAG	ATCAGAAAGA	ATCTCTCCCA	ACATTTTAGA	GTCTTGCTTC
1701	CCAAACCAGA	AAAAGTCAGA	CTCATTGTTG	ATTTAAAACT	TTTAACATTT
1751	TGTTTGGCTG	GATTGTACTA	CTTTACCTCT	ACTTTACCAC	CACCACCCTT
1801	TTCTCCCTC	CTTTCCAAAT	AATATACAGA	ACTCCAAAAT	AGCTTCATTT
1851	AAGGATTTTT	TTGTGAGTTA	ACAATTTCT	TGAAATCCTG	TGAAATAGAT
1901	TTGCACAGAC	ACCTTGTGAG	TGATTGGTAT	TGGAGGTGTT	CAAGAAACTG
1951	TTCGAAAAAG	AACAAAAACA	CTTCCCTCGT	TATTTTCTCT	CATTTTTTGA
2001	TGAGAGGAAA	ATTTGAAACA	TTATTCTTGT	TGTTGTTGGT	AATAGCATAA
2051	TGACAGTGGG	AGGGGTACAA	GGGGATAAGA	AAAATGTCAT	GATTTTTTTC
2101	CGGTCCTGCC	ACATGTAACA	CTTACTCTGT	TACCTAAATT	TTATAGTTAG
2151	ATCATATCCA	ATCTACTTAT	TAAACTGTGT	TCTATTTACC	AGTGGAGTTT
2201	TTCTGCAGTG	GTTGCGTTTC	ACTGTAAGGA	TAATGGAGTT	CCTCTCCTCT
2251	GCTTTCCTCA	GAGGATGGTC	CTTTAACATA	GCCAGAAACA	AGCCCTGTGG
2301	TTTGAAGGTG	AGCTGTGAGG	ATGGGACTAA	TTGATATGCA	CCAGTTTACA
2351	AAGACAGTCT	TATCATCCGA	GAATACACCA	TCTTTTTCTC	TGGATAATTA
2401	TTTCTTACAT	CATGCTTGAT	TCCTACATTT	TGTTGGGTTT	CAACATTGGC
2451	TCAGGAATGC	TGTTAATATT	TATTCTGTAT	TGATAAAAAG	TCTGTCTTGC
2501	CACTACAAGT	AAATCCCCCA	TTTAATATTT	TCTTCTTTAG	CATAGCACTG
2551	TCATTTTTTG	TGAAAATGGT	TATGTTTATT	TATTACAATA	CTGAGTCATA
2601	TATAAATTTT	CAATAAAAGC	AGAAACTTTC	TTACCTTAAA	AAAAAAAAAA
2651	AAAAAAAAAA	AAAAAAA			

INFORMATION OF SEQ ID-NO:2

SEQUENCE CHARACTERISTICS:

LENGTH: 2547 base pairs
SPECIES: desoxyribonucleic acid
TOPOLOGY: linear

MOLECULE SPECIES: cDNA

HYPOTHETICALLY: no

ANTI-SENSE: no

NATURAL ORIGIN :

ORGANISM: Homo sapiens
STRAIN: caucasian
DEVELOPMENTAL STAGE: adult
CELL TYPE: epidermal keratinocyte

DIRECT ORIGIN: cDNA from keratinocytes

FEATURE:

NAME/KEY: splice variant of a coding
sequence
for the regulatory protein pKe#83
from human keratinocytes

POSITION: from 1 to 2547

METHOD OF INVESTIGATION: cDNA-sequencing

SEQ ID NO: 2

```
1  GTTTTGTTAG  GCAAAAAGAG  ACTATTGAAA  GCTGAGACTT  TAGAATTGAG
51  TGACTIONAT  GTTAGTGATA  AGAAGAAGGA  TATGTCTCCA  CCCTTTATTT
101 GTGAGGAGAC  AGATGAACAA  AAGCTTCAAA  CTCTAGACAT  CGGTAGTAAC
151 TTGGAGAAAG  AAAAATTAGA  GAATTCCAGA  TCCTTAGAAT  GCAGATCAGA
201 TCCAGAATCT  CCTATCAAAA  AAACAAGTTT  ATCTCCTACT  TCTAAACTTG
251 GATACTCATA  TAGTAGAGAT  CTAGACCTTG  CTAAGAAAAA  ACATGCTTCC
301 CTGAGGCAGA  CGGAGTCTGA  TCCAGATGCT  GATAGAACCA  CTTTAAATCA
351 TGCAGATCAT  TCATCAAAAA  TAGTCCAGCA  TCGATTGTTA  TCTAGACAAG
401 AAGAACTTAA  GGAAAGAGCA  AGAGTTCTGC  TTGAGCAAGC  AAGAAGAGAT
451 GCAGCCTTAA  AGGCGGGGAA  TAAGCACAAT  ACCAACACAG  CCACCCCATTT
501 CTGCAACAGG  CAGCTAAGTG  ATCAGCAAGA  TGAAGAGCGA  CGTCGGCAGC
551 TGAGAGAGAG  AGCTCGTCAG  CTAATAGCAG  AAGCTCGATC  TGGAGTGAAG
601 ATGTCAGAAC  TTCCCAGCTA  TGGTGAAATG  GCTGCAGAAA  AGTTGAAAGA
651 AAGGTCAAAG  CAAAACAGTA  AGTTGGTGGA  CTTGAAGCTG  AAGAAGCTCC
701 TAGAAgTTCA  gCCACAGGTG  GCAAATTCaC  CCTCCAGTGC  TGCCCAGAAA
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751	GCTGTA	ACTG	AgAg	CTCa	GA	gCa	GGA	CATG	AAA	AGT	GGCa	CAGA	AGAT	CT
801	CCGGAC	TGAA	CGATT	ACAAA		AAACA	ACAGA		ACG	TTTT	TAGA	AATC	CTGT	TG
851	TGTTCA	GCAA	AGATT	CTACA		GTCA	GAAAA		CTCA	ACT	TCA	GTCT	TTCA	GC
901	CAATAT	ATTG	AGAAT	AGACC		AGAG	ATGAAA		AGGC	AGAG	AT	CAAT	ACAG	GA
951	AGATAC	AAAG	AAAGG	AAATG		AGGAG	AAGGC		AGCG	ATA	ACT	GAA	ACTC	AG
1001	GGAAGC	CATC	AGAAG	ATGAA		GTGCT	TAATA		AAGG	GT	TCAA	AGAC	ACC	AGT
1051	CAGTAT	GTAG	TAGG	AGAATT		GGCAG	CACTA		GAGA	AT	GAGC	AAA	AGCA	AAT
1101	TGACAC	CCCGT	GCCG	CGCTG	G	TGGAG	AAGCG		CCTT	CG	CTAT	CTCA	TGG	ACA
1151	CAGGA	AAGGAA	CACAG	AAGAA		GAAGA	AAGCTA		TGAT	GC	AGGA	ATGG	TTT	ATG
1201	TTAGTT	AAATA	AGAAAA	ATGC		CTTA	ATAAGG		AGA	AT	GAA	AGCT	CTCT	CT
1251	TCTGGA	AAAAA	GAAC	ATGATT		TAGA	ACGACG		GTAT	GAG	CTG	CTGA	ACC	GGG
1301	AATTGA	GGGGC	AATG	CTAGCC		ATTGA	AAGACT		GGC	AGA	AAGAC	CGAG	GCCC	AG
1351	AAGCGA	CGCG	AACAG	CTTCT		GCTAG	ATGAG		CTGG	TGG	CCCC	TGGT	GAA	CAA
1401	GCGCGA	TGCG	CTCG	TCA	GGG	ACCT	GGA	CGC	GC	AGG	AGA	AAG	CCCA	GAG
1451	AAGAAG	ATGA	GCATT	TGGAG		CGAA	CTCTG	G	AGC	AAA	ACAA	AGG	CAAG	ATG
1501	GCCAAG	AAAAG	AGGAG	AAAATG		TGTT	CTTCAG		TAG	CC	ATCAG	ATC	AGAA	AGA
1551	ATCTCT	CCCA	ACATT	TTTAGA		GTCT	TGCTTC		CCA	A	ACCAGA	AAA	AGT	CAGA
1601	CTCATT	GTGTG	ATTTA	AAAACT		TTTA	ACATTT		TGTT	TGG	CTG	GATT	GT	ACTA
1651	CTTTAC	CTCT	ACTTT	ACCAC		CACC	ACCCTT		TTCC	TCC	CTC	CTTT	CCAA	AT
1701	AATATA	CAGA	ACTCC	AAAAT		AGCT	TCATTT		AAGG	ATTTT	TT	TGTG	AG	TTA
1751	ACAATT	TCCT	TGAA	ATCCTG		TGAA	ATAGAT		TTGC	ACAG	AC	ACCT	TGT	GAG
1801	TGATTG	GTAT	TGGAG	GTGT		CAAG	AAACTG		TTCG	AAAA	AAG	AAC	AAAA	ACA
1851	CTTCC	CTCGT	TATTT	TCTCT		CATTT	TTTGA		TGAG	AGG	AAA	ATTT	GAA	ACA
1901	TTATT	CTTGT	TGTT	TGTTGGT		AATAG	CATAA		TGAC	AGT	TGGG	AGGG	G	TACAA
1951	GGGGAT	AAGA	AAAAT	GT	CAT	GATTT	TTTTTC		CGGT	CCT	GCC	ACAT	G	TAA
2001	cTTAc	TcTGT	TACCT	AAATT		TTAT	AGTTAG		ATCA	TAT	CCa	ATc	tACT	TAT
2051	TAAACT	GTGT	TCTAT	TTTACC		AGTGG	AGTTT		TTc	TGC	AGTG	Gt	TGCG	TTT
2101	ACTGTA	AAGGA	TAATG	GAGTT		CcTc	TcTcTCT		GCTTT	CCT	CA	GAGG	AT	G
2151	CTTTA	AcATA	GCCAG	AAACA		AGCC	CTGTGG		TTTGA	AGGTG		AGCT	GTG	AGG
2201	ATGGGA	CTAA	TTGAT	ATGCA		CCAG	TtACA		AAG	ACAGT	cT	Ta	T	CCGA
2251	GAAt	ACACCA	TcTTTT	TcTc		TGG	ATAATTA		TTTCT	tACAT		CATG	CTT	GAT
2301	TCCT	ACATTT	TGTT	GGGTTT		CAAC	ATTGGC		TCAC	G	AATGC	TGTT	AA	tATT
2351	TATTCT	GTAT	tGATA	AAAAAG		TcTGT	cTTGC		CACT	ACA	AGT	AAAT	CCCC	CA
2401	TTTAAT	ATTTT	TcTTc	TTTAG		CATAG	CACTG		TCAT	TTTTTT	TG	TGAA	AAT	GGT
2451	TATGTT	TATT	TATTA	CAATA		CTGAG	T	CATA	TATA	AATTTT		CAATA	AAA	AGC
2501	AGAA	ACTTTC	TTAC	CTTAAA		AAAA	AAAAAA		AAAA	AAAAAA		AAAA	AAAA	

INFORMATION OF SEQ ID-NO:3

SEQUENCE CHARACTERISTICS:

LENGTH: 523 amino acids
SPECIES: amino acid sequence

MOLECULE SPECIES: protein

NATURAL ORIGIN :

ORGANISM: Homo sapiens
STRAIN: caucasian
DEVELOPMENTAL STAGE: adult
CELL TYPE: epidermal keratinocyte

DIRECT ORIGIN: derived of cDNA sequence

FEATURE:

NAME/KEY: coding sequence
for the regulatory protein pKe#83
from human Keratinocytes

POSITION: from 1 to 523
METHOD OF INVESTIGATION: derivation of cDNA sequence
FURTHER INFORMATION: comprises a prenyl-group binding
site („CAAX box“), nine protein
kinase phosphorylation motives, and
two tyrosine kinase phosphorylation
motives

SEQ ID NO: 3

```
1  MSPPFICEET DEQKLQTLDI GSNLEKEKLE NSRSLECRSD PESPIKKTSL
51  SPTSKLGYSY SRDLDLAKKK HASLRQTESD PDADRTTLNH ADHSSKIVQH
101 RLLSRQEELK ERARVLLEQA RRDAALKAGN KHNTNTATPF CNRQLSDQQD
151 EERRRQLRER ARQLIAEARS GVKMSELPSY GEMAAEKLKE RSKASGDEND
201 NIEIDTNEEI PEGFVVGGGD ELTNLENDLD TPEQNSKLVD LKLKKLLEVQ
251 PQVANSPSSA AQKAVTESSE QDMKSGTEDL RTERLQKTTE RFRNPVVFSK
301 DSTVRKTQLQ SFSQYIENRP EMKRQRSIQE DTKKGNEEKA AITETQRKPS
351 EDEVLNKGFK DTSQYVVGEL AALENEQKQI DTRAALVEKR LRYLMDTGRN
401 TEEEEAMMQE WFMLVNKKNA LIRRMNQLSL LEKEHDLERR YELLNRELRA
451 MLAIEDWQKT EAQKRREQLL LDELVALVNK RDALVRDLDA QEKQAEDEDE
```

501 HLERTLEQNK GKMAKKEEK VLQ*

INFORMATION OF SEQ ID-NO:4

SEQUENCE CHARACTERISTICS:

LENGTH: 482 amino acids
SPECIES: amino acid sequence

MOLECULE SPECIES: protein

NATURAL ORIGIN :

ORGANISM: Homo sapiens
STRAIN: caucasian
DEVELOPMENTAL STAGE: adult
CELL TYPE: epidermal keratinocyte

DIRECT ORIGIN: derived of cDNA sequence

FEATURE:

NAME/KEY: coding sequence for the
regulatory protein pKe#83
from human keratinocytes

POSITION: from 1 to 482
METHOD OF INVESTIGATION: derivation of cDNA sequence
FURTHER INFORMATION: comprises a prenyl-group binding
site („CAAX box“) , nine protein
kinase phosphorylation motives,

15

casein kinase phosphorylation
motives and two tyrosine kinase
phosphorylation motives

SEQ ID NO: 4

```
1  MSPPFICEET DEQKLQTLDI GSNLEKEKLE NSRSLECRSD PESPIKKTSL
51  SPTSKLGYSY SRDLDLAKKK HASLRQTESD PDADRTTLNH ADHSSKIVQH
101 RLLSRQEELK ERARVLLEQA RRDAALKAGN KHNTNTATPF CNRQLSDQQD
151 EERRRQLRER ARQLIAEARS GVKMSELPY GEMAAEKLKE EQNSKLVDLK
201 LKKLLEVQPQ VANSPSSAAQ KAVTESSEQD MKSGTEDLRT ERLQKTTERF
251 RNPVVFSKDS TVRKTQLQSF SQYIENRPEM KRQRSIQEDT KKGNEEKAAI
301 TETQRKPSER EVLNKGFKDT SQYVVGELAA LENEQKQIDT RAALVEKRLR
351 YLMDTGRNTE EEEAMMQEWF MLVNKKNALI RRMNQLSLE KEHDLERRYE
401 LLNRELRAML AIEDWQKTEA QKRREQLLLD ELVALVNKRD ALVRDLDAQE
451 KQAEEDDEHL ERTLEQNKGK MAKKEEKCVL Q*
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INFORMATION OF SEQ ID NO:5

SEQUENCE CHARACTERISTICS:

LENGTH: 2559 base pairs
SPECIES: desoxyribonucleic acid
TOPOLOGY: linear

MOLECULE SPECIES: cDNA

HYPOTHETICALLY: no

ANTI-SENSE: no

NATURAL ORIGIN :

ORGANISM: Homo sapiens
STRAIN: caucasian
DEVELOPMENTAL STAGE: adult
CELL TYPE: epidermal keratinocyte

DIRECT ORIGIN: cDNA from keratinocytes

FEATURE:

NAME/KEY: splice variant of a coding
sequence
for the regulatory protein pKe#83
from human keratinocytes

POSITION: from 1 to 2559

METHOD OF INVESTIGATION: cDNA-Sequencing

SEQ ID NO: 5

```
1   GTTTTGTAG GCAAAAAGAG ACTATTGAAA GCTGAGACTT TAGAATTGAG
51  TGACTTATAT GTTAGTGATA AGAAGAAGGA TATGTCTCCA CCCTTTATTT
101 GTGAGGAGAC AGATGAACAA AAGCTTCAAA CTCTAGACAT CGGTAGTAAC
151 TTGGAGAAAG AAAAATTAGA GAATTCAGGA TCCTTAGAAT GCAGATCAGA
201 TCCAGAATCT CCTATCAAAA AAACAAGTTT ATCTCCTACT TCTAAACTTG
251 GATACTCATA TAGTAGAGAT CTAGACCTTG CTAAGAAAAA ACATGCTTCC
301 CTGAGGCAGA CGGAGTCTGA TCCAGATGCT GATAGAACCA CTTTAAATCA
351 TGCAGATCAT TCATCAAAAA TAGTCCAGCA TCGATTGTTA TCTAGACAAG
401 AAGAACTTAA GGAAAGAGCA AGAGTTCTGC TTGAGCAAGC AAGAAGAGAT
451 GCAGCCTTAA AGGCGGGGAA TAAGCACAAT ACCAACACAG CCACCCCAT
501 CTGCAACAGG CAGCTAAGTG ATCAGCAAGA TGAAGAGCGA CGTCGGCAGC
551 TGAGAGAGAG AGCTCGTCAG CTAATAGCAG AAGCTCGATC TGGAGTGAAG
601 ATGTCAGAAC TTCCCAGCTA TGGTGAAATG GCTGCAGAAA AGTTGAAAGA
651 AAGGTCAAAG GCATCTGGAG AACAAAACAG TAAGTTGGTG GACTTGAAGC
701 TGAAGAAGCT CCTAGAAGTT CAGCCACAGG TGGCAAATTC ACCCTCCAGT
751 GCTGCCCAGA AAGCTGTAAC TGAGAGCTCA GAGCAGGACA TGAAGAGTGG
801 CACAGAAGAT CTCCGGACTG AACGATTACA AAAACAACA GAACGTTTAA
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851 GAAATCCTGT TGTGTTTCAGC AAAGATTCTA CAGTCAGAAA AACTCAACTT

901	CAGTCTTTCA	GCCAATATAT	TGAGAATAGA	CCAGAGATGA	AAAGGCAGAG
951	ATCAATACAG	GAAGATACAA	AGAAAGGAAA	TGAGGAGAAG	GCAGCGATAA
1001	CTGAAACTCA	GAGGAAGCCA	TCAGAAGATG	AAGTGCTTAA	TAAAGGGTTC
1051	AAAGACACCA	GTCAGTATGT	AGTAGGAGAA	TTGGCAGCAC	TAGAGAATGA
1101	GCAAAAGCAA	ATTGACACCC	GTGCCGCGCT	GGTGGAGAAG	CGCCTTCGCT
1151	ATCTCATGGA	CACAGGAAGG	AACACAGAAG	AAGAAGAAGC	TATGATGCAG
1201	GAATGGTTTA	TGTTAGTTAA	TAAGAAAAAT	GCCTTAATAA	GGAGAATGAA
1251	TCAGCTCTCT	CTTCTGGAAA	AAGAACATGA	TTTAGAACGA	CGGTATGAGC
1301	TGCTGAACCG	GGAATTGAGG	GCAATGCTAG	CCATTGAAGA	CTGGCAGAAG
1351	ACCGAGGCC	AGAAGCGACG	CGAACAGCTT	CTGCTAGATG	AGCTGGTGGC
1401	CCTGGTGAAC	AAGCGCGATG	CGCTCGTCAG	GGACCTGGAC	GCGCAGGAGA
1451	AGCAGGCCGA	AGAAGAAGAT	GAGCATTTGG	AGCGAACTCT	GGAGCAAAAC
1501	AAAGGCAAGA	TGGCCAAGAA	AGAGGAGAAA	TGTGTTCTTC	AGTAGCCATC
1551	AGATCAGAAA	GAATCTCTCC	CAACATTTTA	GAGTCTTGCT	TCCCAAACCA
1601	GAAAAAGTCA	GACTCATTGT	TGATTTAAAA	CTTTTAACAT	TTTGTTTGGC
1651	TGGATTGTAC	TACTTTACCT	CTACTTTACC	ACCACCACCC	TTTTCTCCC
1701	TCCTTTCCAA	ATAATATACA	GAAC TCCAAA	ATAGCTTCAT	TTAAGGATTT
1751	TTTTGTGAGT	TAACAATTTC	CTTGAAATCC	TGTGAAATAG	ATTTGCACAG
1801	ACACCTTGTG	AGTGATTGGT	ATTGGAGGTG	TTCAAGAAAC	TGTTCGAAAA
1851	AGAACAAAAA	CACTTCCCTC	GTTATTTTCT	CTCATTTTTT	GATGAGAGGA
1901	AAATTTGAAA	CATTATTCTT	GTTGTTGTTG	GTAATAGCAT	AATGACAGTG
1951	GGAGGGGTAC	AAGGGGATAA	GAAAAATGTC	ATGATTTTTT	TCCGGTCCTG
2001	CCACATGTAA	CACTTACTCT	GTTACCTAAA	TTTTATAGTT	AGATCATATC
2051	CAATCTACTT	ATTAAACTGT	GTTCTATTTA	CCAGTGGAGT	TTTTCTGCAG
2101	TGGTTGCGTT	TCACTGTAAG	GATAATGGAG	TTCCTCTCCT	CTGCTTTCCT
2151	CAGAGGATGG	TCCTTTAACA	TAGCCAGAAA	CAAGCCCTGT	GGTTTGAAGG
2201	TGAGCTGTGA	GGATGGGACT	AATTGATATG	CACCAGTTTA	CAAAGACAGT
2251	CTTATCATCC	GAGAATACAC	CATCTTTTTC	TCTGGATAAT	TATTTCTTAC
2301	ATCATGCTTG	ATTCCTACAT	TTTGTTGGGT	TTCAACATTG	GCTCACGAAT
2351	GCTGTTAATA	TTTATTCTGT	ATTGATAAAA	AGTCTGTCTT	GCCACTACAA
2401	GTAAATCCCC	CATTTAATAT	TTTCTTCTTT	AGCATAGCAC	TGTCATTTTT
2451	TGTGAAAATG	GTTATGTTTA	TTTATTACAA	TACTGAGTCA	TATATAAATT
2501	TTCAATAAAA	GCAGAACTT	TCTTACCTTA	AAAAAAAAAA	AAAAAAAAAA
2551	AAAAAAAAAA				

INFORMATION OF SEQ ID-NO: 6

SEQUENCE CHARACTERISTICS:

LENGTH: 487 amino acids
SPECIES: amino acid sequence

MOLECULE SPECIES: protein

NATURAL ORIGIN :

ORGANISM: Homo sapiens
STRAIN: caucasian
DEVELOPMENTAL STAGE: adult
CELL TYPE: epidermal keratinocyte

DIRECT ORIGIN: derived of cDNA sequence

FEATURE:

NAME/KEY: coding sequence
for the regulatory protein pKe#83
from human Keratinocytes

POSITION: from 1 to 487
METHOD OF INVESTIGATION: derivation of cDNA sequence
FURTHER INFORMATION: comprises a prenyl-group binding
site („CAAX box“), eight protein
kinase phosphorylation motives,
12 casein kinase phosphorylation
motives and two tyrosine kinase
phosphorylation motives

SEQ ID NO: 6

```
1  MSPPFICEET DEQKLQTLDI GSNLEKEKLE NSRSLECRSD PESPIKKTSL
51  SPTSKLGYSY SRDLDLAKKK HASLRQTESD PDADRTTLNH ADHSSKIVQH
101 RLLSRQEELK ERARVLEQA RRDAALKAGN KHNTNTATPF CNRQLSDQQD
151 EERRRQLRER ARQLIAEARS GVKMSELPY GEMAAEKLKE RSKASGEQNS
201 KLVDLKLKKL LEVQPQVANS PSSAAQKAVT ESSEQDMKSG TEDLRTERLQ
251 KTTERFRNPV VFSKDSTVRK TQLQSFSQYI ENRPEMKRQR SIQEDTKKGN
301 EEKAAITETQ RKPSEDEVLN KGFKDTSQYV VGELAALENE QKQIDTRAAL
351 VEKRLRYLMD TGRNTEEEEA MMQEWFMLVN KKNALIRRMN QLSLLEKEHD
401 LERRYELLNR ELRAMLAIED WQKTEAQKRR EQLLLDELVA LVNKRDALVR
451 DLDAQEKQAE EEDEHLERTL EQNKGKMAKK EEKCVLQ*
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INFORMATION OF SEQ ID NO 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 4911 base pairs
SPECIES: desoxyribonucleic acid
TOPOLOGY: linear

MOLECULE SPECIES: cDNA

HYPOTHETICALLY: no

ANTI-SENSE: no

NATURAL ORIGIN :

ORGANISM: Homo sapiens
STRAIN: caucasian
DEVELOPMENTAL STAGE: adult
CELL TYPE: epidermal keratinocyte

DIRECT ORIGIN: cDNA from keratinocytes

FEATURE:

NAME/KEY: coding sequence for the
regulatory protein pKe#83
from human keratinocytes

POSITION: from 1 to 4911
METHOD OF INVESTIGATION: cDNA-sequencing

SEQ ID NO 7:

```
1  GCGGGGGGAG CCCTCCAGAA TACCCATCAT ATAGCCCCTG AGGTGGCATG
51  GTGATGTCTC CATGAGGGAA CCCCTTCCCA CTTCATACTG TCACGTATAT
101 CATAGTGTTT TTGACTGGGC CATTCACTA AGATGGGATT TACCCTGTGA
151 AACAGGGAGA AGACTTATGG ACCCCAAGCA TCATTTCAAG TTGAAGTTGA
201 GTTTTTAAAA GCCATCCATG CAAAGTTCCT TTGCTTTGGA CCCTCTGCAT
251 TATTAAAGCT GCTGTATTGC TAACCCAGAA CTGCTCCAGT GTCTTGACTG
301 ATCATCATGG CTTCAAGTTG GAAGAGACTG CAGCGTGTGG GAAAACATGC
351 ATCCAAGTTC CAGTTTGTGG CCTCCTACCA GGAGCTCATG GTTGAGTGTA
401 CGAAGAAATG GTAACCAGAT AAAGTGGTGG TAGTTTGGAC CAGAAGAAGC
451 CGAAGGAAGT CTTCTAAGGC ACATAGCTGG CAACCTGGAA TAAAAAATCC
501 CTATCGTGGT GTTGTTGTGT GGCTGTTCCT TGAAAACATT GAAATCACTG
551 TAACACTTTT TAAGGATCCT CATGCGGAAG AATTTGAAGA CAAAGAGTGG
601 ACATTTGTCA TAGAAAATGA ATCCCCTTCT GGTCTGAAGGA AAGCTCTTGC
651 TACTAGCAGC ATCAATATGA AACAGTATGC AAGCCCTATG CCAACTCAGA
701 CTGATGTCAA GTTAAATTC AAGCCATTAT CTAAAAAAGT TGTATCTGCC
751 GCTCTTCAGT TTTCATTATC TTGCATTTT CTGAGGGAAG GAAAAGCCAC
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801	AGATGAAGAC	ATGCAAAGTT	TGGCTAGTTT	GGTGAGTATG	AAGCAGGCTG
851	ACATTGGCAA	TTTAGATGAC	TTCGAAGAAG	ATAATGAAGA	TGATGATGAG
901	AACAGAGTGA	ACCAAGAAGA	AAAGGCAGCT	AAAATTACAG	AGCTTATCAA
951	CAAACCTAAC	TTTTTGGATG	AAGCAGAAAA	GGACTTGGCC	ACCGTGAATT
1001	CAAATCCATT	TGATGATCCT	GATGCTGCAG	AATTAAATCC	ATTTGGAGAT
1051	CCTGACTCAG	AAGAACCTAT	CACTGAAACA	GCTTCACCTA	GAAAAACAGA
1101	AGACTCTTTT	TATAATAACA	GCTATAATCC	CTTTAAAGAG	GTGCAGACTC
1151	CACAGTATTT	GAACCCATTC	GATGAGCCAG	AAGCATTTGT	GACCATAAAG
1201	GATTCTCCTC	CCCAGTCTAC	AAAAAGAAAA	AATATAAGAC	CTGTGGATAT
1251	GAGCAAGTAC	CTCTATGCTG	ATAGTTCTAA	AACTGAAGAA	GAAGAATTGG
1301	ATGAATCAAA	TCCTTTTTTAT	GAACCTAAAT	CAACTCCTCC	TCCAAATAAT
1351	TTGGTAAATC	CTGTTCAAGA	ACTAGAAACT	GAAAGGCGAG	TGAAAAGAAA
1401	GGCCCCGGCT	CCACCAGTCC	TCTCACCAAA	AACAGGAGTA	TAAATGAAA
1451	ACACAGTTTC	TGCAGGAAAA	GATCTCTCTA	CTTCTCCTAA	GCCAAGCCCT
1501	ATACCAAGTC	CTGTTTTGGG	GCGAAAGCCA	AATGCTAGTC	AGTCTTTGCT
1551	TGTATGGTGT	AAAGAAGTTA	CAAAGAACTA	CCGAGGAGTA	AAAATCACCA
1601	ATTTTACTAC	ATCGTGGAGA	AATGGTTTAT	CTTTTTGTGC	AATATTACAC
1651	CACTTTAGAC	CAGATTTAAT	TGACTACAAG	TCTCTGAATC	CTCAAGATAT
1701	TAAAGAGAAC	AACAAAAAGG	CATACGATGG	ATTTGCCAGC	ATAGGAATTT
1751	CCCGATTATT	GGAACCTTCT	GATATGGTAT	TATTAGCAAT	TCCTGATAAA
1801	CTGACTGTTA	TGACTTATCT	CTATCAAATA	AGGGCACATT	TCAGTGGCCA
1851	AGAACTAAAT	GTCGTTCAGA	TAGAGGAAAA	CAGCAGTAAA	AGCACATATA
1901	AAGTTGGAAA	CTATGAAACA	GATACAAACA	GTTCTGTTGA	TCAAGAAAAA
1951	TTCTATGCAG	AGCTTAGTGA	TCTGAAGCGG	GAGCCTGAAC	TACAACAGCC
2001	TATCAGCGGA	GCAGTAGACT	TCTTATCACA	GGATGACTCT	GTATTTGTAA
2051	ATGATAGCGG	GGTTGGAGAG	TCAGAAAGTG	AGCATCAAAC	TCCTGATGAT
2101	CACCTTAGTC	CAAGCACAGC	CTCCCCTTAC	TGTCGCAGGA	CTAAAAGTGA
2151	CACAGAACCC	CAGAAGTCTC	AGCAGAGCTC	TGGAAGGACT	TCAGGATCTG
2201	ATGACCCTGG	AATATGTTCC	AATACAGATT	CAACCCAAGC	ACAGGTTTTG
2251	TTAGGCAAAA	AGAGACTATT	GAAAGCTGAG	ACTTTAGAAT	TGAGTGACTT
2301	ATATGTTAGT	GATAAGAAGA	AGGATATGTC	TCCACCCTTT	ATTTGTGAGG
2351	AGACAGATGA	ACAAAAGCTT	CAAACCTAG	ACATCGGTAG	TAACTTGAG
2401	AAAGAAAAAT	TAGAGAATTC	CAGATCCTTA	GAATGCAGAT	CAGATCCAGA
2451	ATCTCCTATC	AAAAAAACAA	GTTTATCTCC	TACTTCTAAA	CTTGGATACT
2501	CATATAGTAG	AGATCTAGAC	CTTGCTAAGA	AAAAACATGC	TTCCCTGAGG
2551	CAGACGGAGT	CTGATCCAGA	TGCTGATAGA	ACCACTTTAA	ATCATGCAGA
2601	TCATTTCATCA	AAAATAGTCC	AGCATCGATT	GTTATCTAGA	CAAGAAGAAC
2651	TTAAGGAAAG	AGCAAGAGTT	CTGCTTGAGC	AAGCAAGAAG	AGATGCAGCC
2701	TTAAAGGCGG	GGAATAAGCA	CAATACCAAC	ACAGCCACCC	CATTCTGCAA
2751	CAGGCAGCTA	AGTGATCAGC	AAGATGAAGA	GCGACGTCGG	CAGCTGAGAG
2801	AGAGAGCTCG	TCAGCTAATA	GCAGAAGCTC	GATCTGGAGT	GAAGATGTCA
2851	GAACCTCCCA	GCTATGGTGA	AATGGCTGCA	GAAAAGTTGA	AAGAAAGGTC
2901	AAAGGCATCT	GGAGATGAAA	ATGATAATAT	TGAGATAGAT	ACTAACGAGG
2951	AGATCCCTGA	AGGCTTTGTT	GTAGGAGGTG	GAGATGAACT	TACTAACTTA
3001	GAAAATGACC	TTGATACTCC	CGAACAAAAC	AGTAAGTTGG	TGGACTTGAA
3051	GCTGAAGAAG	CTCCTAGAAG	TTCAGCCACA	GGTGGCAAAT	TCACCCTCCA
3101	GTGCTGCCCC	GAAAGCTGTA	ACTGAGAGCT	CAGAGCAGGA	CATGAAAAGT
3151	GGCACAGAAG	ATCTCCGGAC	TGAACGATTA	CAAAAAACAA	CAGAACGTTT
3201	TAGAAATCCT	GTTGTGTTCA	GCAAAGATTC	TACAGTCAGA	AAAACCTAAC
3251	TTCAGTCTTT	CAGCCAATAT	ATTGAGAATA	GACCAGAGAT	GAAAAGGCAG
3301	AGATCAATAC	AGGAAGATAC	AAAGAAAGGA	AATGAGGAGA	AGGCAGCGAT
3351	AACTGAAACT	CAGAGGAAGC	CATCAGAAGA	TGAAGTGCTT	AATAAAGGGT

3401	TCAAAGACAC	CAGTCAGTAT	GTAGTAGGAG	AATTGGCAGC	ACTAGAGAAT
3451	GAGCAAAAGC	AAATTGACAC	CCGTGCCGCG	CTGGTGGAGA	AGCGCCTTCG
3501	CTATCTCATG	GACACAGGAA	GGAACACAGA	AGAAGAAGAA	GCTATGATGC
3551	AGGAATGGTT	TATGTTAGTT	AATAAGAAAA	ATGCCTTAAT	AAGGAGAATG
3601	AATCAGCTCT	CTCTTCTGGA	AAAAGAACAT	GATTTAGAAC	GACGGTATGA
3651	GCTGCTGAAC	CGGGAATTGA	GGGCAATGCT	AGCCATTGAA	GACTGGCAGA
3701	AGACCGAGGC	CCAGAAGCGA	CGCGAACAGC	TTCTGCTAGA	TGAGCTGGTG
3751	GCCCTGGTGA	ACAAGCGCGA	TGCGCTCGTC	AGGGACCTGG	ACGCGCAGGA
3801	GAAGCAGGCC	GAAGAAGAAG	ATGAGCATTT	GGAGCGAACT	CTGGAGCAAA
3851	ACAAAGGCAA	GATGGCCAAG	AAAGAGGAGA	AATGTGTTCT	TCAGTAGCCA
3901	TCAGATCAGA	AAGAATCTCT	CCCAACATTT	TAGAGTCTTG	CTTCCCAAAC
3951	CAGAAAAAGT	CAGACTCATT	GTTGATTTAA	AACTTTTAAC	ATTTTGT TTG
4001	GCTGGATTGT	ACTACTTTAC	CTCTACTTTA	CCACCACCAC	CCTTTTCTCTC
4051	CCTCCTTTCC	AAATAATATA	CAGAACTCCA	AAATAGCTTC	ATTTAAGGAT
4101	TTTTTTGTGA	GTTAACAATT	TCCTTGAAAT	CCTGTGAAAT	AGATTTGCAC
4151	AGACACCTTG	TGAGTGATTG	GTATTGGAGG	TGTTCAAGAA	ACTGTTCGAA
4201	AAAGAACAAA	AACACTTCCC	TCGTTATTTT	CTCTCATTTT	TTGATGAGAG
4251	GAAAATTTGA	AACATTATTC	TTGTTGTTGT	TGGTAATAGC	ATAATGACAG
4301	TGGGAGGGGT	ACAAGGGGAT	AAGAAAAATG	TCATGATTTT	TTTCCGGTCC
4351	TGCCACATGT	AACACTTACT	CTGTTACCTA	AATTTTATAG	TTAGATCATA
4401	TCCAATCTAC	TTATTAAACT	GTGTTCTATT	TACCAGTGGA	GTTTTTCTGC
4451	AGTGGTTGCG	TTTCACTGTA	AGGATAATGG	AGTTCCTCTC	CTCTGCTTTC
4501	CTCAGAGGAT	GGTCCTTTAA	CATAGCCAGA	AACAAGCCCT	GTGGTTTGAA
4551	GGTGAGCTGT	GAGGATGGGA	CTAATTGATA	TGCACCAGTT	TACAAAGACA
4601	GTCTTATCAT	CCGAGAATAC	ACCATCTTTT	TCTCTGGATA	ATTATTTCTT
4651	ACATCATGCT	TGATTCCTAC	ATTTTGT TGG	GTTTCAACAT	TGGCTCACGA
4701	ATGCTGTTAA	TATTTATTCT	GTATTGATAA	AAAGTCTGTC	TTGCCACTAC
4751	AAGTAAATCC	CCCATTTAAT	ATTTTCTTCT	TTAGCATAGC	ACTGTCA TTT
4801	TTTGTGAAAA	TGGTTATGTT	TATTTATTAC	AATACTGAGT	CATATATAAA
4851	TTTTCAATAA	AAGCAGAAAC	TTTCTTACCT	TAAAAAAAAA	AAAAAAAAAA
4901	AAAAAAAAAA	A*			

(END)

INFORMATION OF SEQ ID-NO:8

SEQUENCE CHARACTERISTICS:

LENGTH: 1076 amino acids
SPECIES: amino acid sequence

MOLECULE SPECIES: protein

NATURAL ORIGIN :

ORGANISM: Homo sapiens
STRAIN: caucasian
DEVELOPMENTAL STAGE: adult
CELL TYPE: epidermal keratinocyte

DIRECT ORIGIN: derived of cDNA sequence

FEATURE:

NAME/KEY: coding sequence for the
regulatory protein pKe#83
from human keratinocytes
POSITION: from 1 to 1076

METHOD OF INVESTIGATION: derivation of cDNA sequence
FURTHER INFORMATION: comprises a prenyl-group binding
site („CAAX box“) , 24 protein
kinase phosphorylation motives,

29

casein kinase phosphorylation
motives, 5 tyrosine kinase
phosphorylation motives and
8 Myrsitylation sites

SEQ ID-NO. 8:

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1  MKQYASPMPT QTDVCLKFKP LSKKVVSAAAL QFSLSCIFLR EGKATDEDMQ
51  SLASLVSMKQ ADIGNLDDFE EDNEDDDENR VNQEEKAAKI TELINKLNFL
101 DEAEKDLATV NSNPFDDPDA AELNPFDPD SEEPITETAS PRKTEDSFYN
151 NSYNPFKEVQ TPQYLNPFDE PEAFTIKDS PPQSTKRKNI RPDVMSKYLY
201 ADSSKTEEEE LDESNPFYEP KSTPPPNLV NPVQELTER RVKRKAPAPP
251 VLSPKTGVLN ENTVSAGKDL STSPKPSPIP SPVLGRKPNA SQSLLVWCKE
301 VTKNYRGVKI TNFTTSWRNG LSFCAILHHF RPDLDYKSL NPQDIKENNK
351 KAYDGFASIG ISRLLEPSDM VLLAIPDKLT VMTYLYQIRA HFSGQELNVV
401 QIEENSSTST YKVGNYETDT NSSVDQEKFY AELSDLKREP ELQQPISGAV
451 DFLSQDDSVF VNDSGVGESE SEHQTPDDHL SPSTASPYCR RTKSDTEPQK
501 SQQSSGRTSG SDDPGICSNT DSTQAQVLLG KKRLKAETL ELSDLYVSDK
551 KKDMSPPFIC EETDEQKLQT LDIGSNLEKE KLENSRSLEC RSDPESPIKK
601 TSLSPSTKLG YSYSRDLDA KKKHASLRQT ESDPDADRTT LNHADHSSKI
651 VQHRLLSRQE ELKERARVLL EQARRDAALK AGNKHNTNTA TPFCNRQLSD
701 QQDEERRRQL RERARQLIAE ARSGVKMSEL PSYGEMAAEK LKERSKASGD
751 ENDNIEIDTN EEIPEGFVVG GGDELTNLEN DLDTPQNSK LVDLKLKLL
801 EVQPQVANSF SSAAQKAVTE SSEQDMKSGT EDLRTERLQK TTERFRNPVV
851 FSKDSTVRKT QLQSFSQYIE NRPEMKRQRS IQEDTKKGNE EKAAITETQR
901 KPSEDEVLNK GFKDTSQYVV GELAALENEQ KQIDTRAALV EKRLRYLMDT
951 GRNTEEEAM MQEWFMLVNK KNALIRRMNQ LSLLEKEHDL ERRYELLNRE
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1001 LRAMLAIEDW QKTEAQRRE QLLDELVAL VNKRDALVRD LDAQEKQAE
1051 EDEHLERTLE QNKGKMAKKE EKCVLQ*